Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION
1_____Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2_____Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 J Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4_____Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5_____Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6_____PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7_____Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8_____Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9_____Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10_____Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11_____Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12_____PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

SERIAL NUMBER: 09/549,096

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/549,096

DATE: 07/05/2001
TIME: 16:28:38

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07032001\I549096.raw

Does Not Comply
Corrected Diskette Needed

```
      2 <110> APPLICANT: Ware, Carl F.
      4 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND METHODS
OF USE
      6 <130> FILE REFERENCE: 051501/0276397
      8 <140> CURRENT APPLICATION NUMBER: 09/549,096
      9 <141> CURRENT FILING DATE: 2000-04-12
     11 <160> NUMBER OF SEQ ID NOS: 6
     13 <170> SOFTWARE: PatentIn Ver. 2.0
```

pgs 1-3

ERRORED SEQUENCES

```
     61 <210> SEQ ID NO: 5
     62 <211> LENGTH: 1169
     63 <212> TYPE: DNA
     64 <213> ORGANISM: Homo sapiens
     66 <220> FEATURE:
     67 <221> NAME/KEY: CDS
     68 <222> LOCATION: (49)..(771)
     70 <400> SEQUENCE: 5
     71 gaggttgaag gacccaggcg tgtcagccct gctccagaga ccttgggc atg gag gag  57
     72 Met Glu Glu                                                      1
W--> 73
     74 agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc   105
     75 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile
W--> 76 5                   10                  15
W--> 77 ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg   153
E--> 78 Phe thr arg Leu gly arg ser his arg arg gln ser cys ser val
W--> 79 25                  30                  35
W--> 80 ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg   201
E--> 81 gly Leu Leu Leu Leu Leu met gly ala gly Leu
E--> 82 45                  50
E--> 83 gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag   249
     84 Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu
W--> 85 55                  60                  65
E--> 86 atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg   297
     87 Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu
W--> 88 70                  75                  80
E--> 89 ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca   345
     90 Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr
W--> 91 85                  90                  95
W--> 92 gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag   393
E--> 93 ala asn ser ser Leu thr gly ser gly gly Pro Leu Leu trp glu
W--> 94 105                 110                 115
W--> 95 gcc ttc ctg agg ggc ctc agc tac cac gat ggg   441
W--> 96 Ala Phe Leu Arg Gly Leu Ser Tyr His Asp Gly
W--> 97                 120                 125                 130
E--> 98 gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg   489
```

DO NOT use TAB codes ↓ move under respective codons

cca Pro 20 / gcc cgg gtg ggt ctg Ala Arg Val Gly Leu 40

What is this? invalid grouping of codons and amino acids

ggg Gly 100 / act cag ctg ggc ctg Thr Gln Leu Gly Leu

also, see item 3 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: US/09/549,096 TIME: 16:28:38

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07032001\I549096.raw

```
     99 Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
W--> 100 135                 140                 145
E--> 101 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc   537
     102 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
W--> 103 150                 155                 160                 cac ggc
W--> 104 ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg   585 His Gly
E--> 105 Leu tyr Lys arg thr Pro arg tyr Pro glu glu Leu glu Leu         165
W--> 106 170                 175                 ttg gtc agc cag cag tca
W--> 107 ccc tgc gga cgg gcc acc agc agc tcc cgg   633 Leu Val Ser Gln Gln Ser
E--> 108 Pro cys gly arg ala thr ser ser ser arg     180                 185
W--> 109 190                 195                 gtc tgg tgg gac agc agc ttc ctg ggt ggt
W--> 110 gtg gta cac ctg gag gct   681 Val Trp Trp Asp Ser Ser Phe Leu Gly Gly
E--> 111 val val his Leu glu ala                   200                 205
E--> 112 210
E--> 113 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg   729
     114 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
W--> 115 215                 220                 225
E--> 116 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga           771
     117 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
W--> 118 230                 235                 240
E--> 119 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag agggtgcctc 831
E--> 120 aggggaaaga aaactcacga agcagaggct gggcgtggtg gctctcgcct gtaatcccag 891
E--> 121 cactttggga ggccaaggca ggcggatcac ctgaggtcag gagttcgaga ccagcctggc 951
E--> 122 taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tggtggtgcc 1011
E--> 123 tgcctgtaat ccagctactc aggaggctga ggcaggataa ttttgcttaa acccgggagg 1071
E--> 124 cggaggttgc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
E--> 125 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaa                        1169
     127 <210> SEQ ID NO: 6
     128 <211> LENGTH: 240
     129 <212> TYPE: PRT
     130 <213> ORGANISM: Homo sapiens
W--> 131 <400> SEQUENCE: 6
     132 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
     133   1               5                  10                  15
     134 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
E--> 135 20                  25                  30
     136 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly
E--> 137 35                  40                  45
     138 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
E--> 139 50                  55                  60
     140 Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
E--> 141 70                  75                  80
     142 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
E--> 143 85                  90                  95
     144 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
E--> 145 100                 105                 110
     146 Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
E--> 147 115                 120                 125
     148 Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
```

Same error

misaligned amino acid nos. (see Item 3 on Error Summary Sheet)

Leu 65

invalid grouping

His Asp 130

RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: US/09/549,096 TIME: 16:28:38

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07032001\I549096.raw

same error

```
E--> 149 135                 140                                 Ser Lys Val Gln Leu Gly
     150 Gly Val Gly Cys Pro Leu Gly Leu Ala Ser                  145                 150
E--> 151 155                 160                 Thr Ile Thr His Gly Leu Tyr Lys Arg Thr
     152 Pro Arg Tyr Pro Glu Glu                                 165                 170
E--> 153 175
     154 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
E--> 155 180                 185                 190
     156 Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
E--> 157 195                 200                 205                             Leu Glu
     158 Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu                  210
E--> 159 215                 220                                 Val Arg Leu Arg Asp Gly
     160 Thr Arg Ser Tyr Phe Gly Ala Phe Met Val                  225                 230
E--> 161 235                 240
     163 ATTORNEY DOCKET NO. 07246/030001
E--> 166 2
```

delete at end of file

All sample Sequence Listing (attached) for valid format

FYI Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doe, Richard
<302> Isolation and Characterization of a Gene Encoding a Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

<400> 1

agctgtagtc attcctgtgt cctcttctct ctgggcttct caccctgcta atcagatctc 60

agggagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120

tgatgtggca attgctggca gtgccacagg cttttcagcc aggcttaggg tgggttccgc 180

cgcggcgcgg cggcccctct cgcgctcctc tcgcgcctct ctctcgctct cctctcgctc 240

Appendix 3, page 2

```
ggacctgatt  aggtgagcag  gaggaggggg  cagttagc      atg  gtt  tca  atg  ttc  agc   296
                                                  Met  Val  Ser  Met  Phe  Ser
                                                    1                   5

ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  ttt  gtt  tgt  ttg  ttc  caa   344
Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
               10                       15                  20

tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt       389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu
          25                       30                  35
```

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2

Met	Val	Ser	Met	Phe	Ser	Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu
1				5					10					15	

Phe	Val	Cys	Leu	Phe	Gln	Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser
			20					25					30		

Leu	Gln	Pro	Asn	Leu
		35		

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3

Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	Ile
1				5					10	

<210> 4
<400> 4
000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by database including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

VERIFICATION SUMMARY DATE: 07/05/2001
PATENT APPLICATION: **US/09/549,096** TIME: 16:28:39

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\07032001\I549096.raw**

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:76 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:78 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:78 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:150 SEQ:5
L:78 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:78 M:112 C: (48) String data converted to lower case,
L:79 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:80 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
M:254 Repeated in SeqNo=5
L:81 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
M:112 Repeated in SeqNo=5
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:92 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:93 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:93 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:94 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:95 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:103 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:105 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:106 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:108 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

VERIFICATION SUMMARY DATE: 07/05/2001
PATENT APPLICATION: **US/09/549,096** TIME: 16:28:39

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\07032001\I549096.raw**

L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1169 Found:1046 SEQ:5
L:131 M:283 W: Missing Blank Line separator, <400> field identifier
L:135 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:139 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:166 M:252 E: No. of Seq. differs, <211>LENGTH:Input:240 Found:171 SEQ:6